

AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph beginning at page 12, lines 3-4, with the following rewritten paragraph:

--Fig. 3A shows the amino acid sequences of 2-hydroxyisoflavanone dehydratases in licorice and soybean (top sequence corresponds to 2-hydroxyisoflavanone dehydratase (licorice) represented by SEQ ID NO: 1; bottom sequence corresponds to 2-hydroxyisoflavanone dehydratase (soybean) represented by SEQ ID NO: 3). --

Please replace the paragraph beginning at page 29, line 11, with the following rewritten paragraph:

-- The cDNA encoding the enzyme was collected, and then the sequence was determined using a sequencer. The cDNA of HIDM (2-hydroxyisoflavanone dehydratase methoxy type) has a 1,178-bp nucleotide and encoded 328 amino acids (Fig. 3A). The search for protein-protein BLAST (~~http://www.ncbi.nlm.nih.gov/BLAST/~~) revealed that an estimated amino acid sequence of licorice HIDM indicates 40% identity with putative proteins of *Arabidopsis thaliana* (Accession NOS: Atlg47480, AT3g48690, and At3g48690), 34% identity with *Nicotiana tabacum* hsr203J (Accession NO: X77136) (Pontier et al., 1994), 31% identity with pea E86 (Accession NO: AB026296) (Ichinose et al., 2001), and 32% identity with carboxylesterase of

Archaeoglobus fulgidus (thermophilic sulfur bacteria) (Accession NO: 1JJIA) (Manco et al., 2000). In addition, the licorice HIDM had the motif of a conserved sequence recorded for carboxylesterases (approximately 40 to 180 amino acids from the N-terminal). --

Please replace the paragraph beginning at page 29, line 11, with the following rewritten paragraph:

-- By retrieving from the expressed sequence tags (ESTs) of soybean (~~http://www.tigr.org/tdb/tgi/gmgi/~~), *Medicago truncatula* (~~http://www.tigr.org/tdb/tgi/mtgi/~~), and *Lotus japonicus* (~~http://www.kazusa.or.jp/en/plant/lotus/EST/~~) (Asamizu et al., 2000), it was revealed that these plants had cDNAs which indicated identity with the licorice HIDM (amino acid identity > 50%). However, those sequences have been annotated as hypothetical proteins. A molecular phylogenetical tree represented that soybean BM177194, *L. japonicus* TC3332, and *M. truncatula* TC43540 proteins form the same branch as that of the dehydratase of licorice (amino acid identity > 80%) (Fig. 3B). The soybean BG456496 has > 60% identity as those of the four proteins, and form the other branch with *M. truncatula* BG456496 (Fig. 3B). --